

CGCTGCTCCCGGCTCTCGGAGGGCCCGCCGCCCTTCGAGTCCGGACTCG
 61 -----+-----+-----+-----+-----+
 GCGACGAGGGCCAGGAGCGCTCCGCGGGCGGGCGGGCGGAGCTCAGGCCTGAGC
 C L L P G P R E A P A A A A F E S G L D -
 120

... 2000 ...

[illegible]

FIG. 1

360

N L N S R T E E T I K F A A A H Y N T E -
 G G I I G G A G T T G A G T T C C T G T C T C T G A T A T T T A A C G A C G C G T G T A T A T T A T G T C

[illegible]

ICTAGACTTTTCATACTATTACTCACCCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T O C M P R E V C -

480

CAATATCTACACCCCTTCTCCTCAAACTCAGCGCTGTTGTGGAAGAATTTGAGGTACAC
I D V G K E ' F G V A T N T F E K P P C V -

540

ACAGGCAGATGTTACACCCCAACGACGTTATCACTCCCGACGTCACGTA

600

CGTGCCTCGATGGAGTCGTTCTGCAATAACTTTAATGTCACCGAGAGAGAGTTCGGGGT
T S Y L S K T L F E I T V P L S O G P K -

650

TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTCACCTAC
P V T I S F A N H T S C R C M S K L D V -

MATCH WITH FIG. 1C

MATCH WITH FIG. 1B

FIG. 1C

661

TTTACAGACAAGTTCATTCATTTATAGACGTTCCCTGCCAGCAACACTACCACAGTGTCT

720

AAATGCTCTGTTCAAGTAAGTAATAATCTGCAAGGACGGTCGTTGTGATGTTGTCACAG

C Y R Q V H S I I R R S L P A T L P Q C Q -

721

AGCAGCGAACAAGACCTGCCCCCAATTTACATGTGGAATAATCACATCTGCAGATGCC

780

TCCGTCGCTTGTCTGACGGGGTGTTAATGTACACCTTATTTAGTGTAGACGTTCTACGG

C A A N K T C P T N Y M W N N H I C R C L -

781

TGGCTCAGGAAGATTTTATGTTTTTCCCTCGATGCTGAGATGACTCAACAGATGATTCC

840

ACCGAGTCCCTTCTAAATAACAAGAAGACCTACGACCTTACTGAGTTGTCTACCTAAGG

C A Q E D F M F S S D A G D D S T D G F H -

841

ATGACATCTGTGACCACAACAAGAGCTGATGAAGAGACCTGTCACTGTCTCTGCAGAG

900

TACTGTAGACACCTGTTGTTCTTCCTCGACCTACTTCTCTGACAGTCAACAGACGTTCTC

C D I C G P N K E L D E E T C Q C V C R A -

901

CGGGCTTCGGCCTGCCAGCTGTGAGACCCACAAGAAGACTAGACAGAACTCATGCCAGT

960

GCCCGAAGCCGGACGGTCCGACACCTGGGGTCTTCTTGATCTGCTTTGAGTACGGTCA

C G L R P A S C G P H K E L D R N S C Q C -

961

GTGCTGTAAAAACAACCTCTTCCCCAGCCCAATGTGGGGCCAACCGAGAATTGATGAAA

1020

CACAGACATTTTGTGTTGAGAGGGGTCGTTACACCCCGGTGGCTCTTAAACTACTT

MATCH WITH FIG. 1D

V C K N K L F P S Q C G A N R E F D E N -
C

T C Q C V C K R T C P R N Q P L N P G K -

C C A C C T E S P Q K C L L K G K K F H -

C H Q T C S C Y R R P C T N R Q K A C E P -

C G F S Y S E E V C R C V P S Y W Q R P Q -

MATCH WITH FIG. 1E

MS*

[illegible]

1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTCTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
71 AGATGAACCTCATGACTGTACTCTACCCAGAATATTGGAATAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
-----+-----+-----+-----+-----+-----+-----+
121 GAAAGGAGGCTGGCAACATTAACAGAGAACAGGCCAACCCTCAACTCAAGGACAGAAAGAGAC
-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
-----+-----+-----+-----+-----+-----+-----+
181 TATAAAATTGCTGCAGCACATTTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTC
-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
-----+-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGAGGTGTGTATAGATGTGGGAAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
-----+-----+-----+-----+-----+-----+-----+
301 CGCGACAACACCTTCTTTAAACCTCCATGTGTCTCCGTCTACAGATGTGGGGTTCCTG
-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C C

FIG. 2A

361 CAATAGTGAGGGCTGCAGTGCATGAACACCAGCAGGCTACCTCAGCAAGACGTTATT
-----+-----+-----+-----+-----+-----+-----+
N S E G L Q C M N T S T S Y L S K T L F
421 TGAATTACAGTGCCTCTCTCTCAAGCCCCAACCAGTAACAATCAGTTTGGCCAATCA
-----+-----+-----+-----+-----+-----+-----+
E I T V P L S Q G P K P V T I S F A N H
481 CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
-----+-----+-----+-----+-----+-----+-----+
T S C R C M S K L D V Y R Q V H S I I R
541 ACGTCCCTGCCAGCACTACCACAGTGTTCAGGCAGCGAACAAGACCTGCCCCACCAA
-----+-----+-----+-----+-----+-----+-----+
R S L P A T L P Q C Q A A N K T C P T N
601 TTACATGTGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTTATGTTTCCTC
-----+-----+-----+-----+-----+-----+-----+
Y M W N N H I C R C L A Q E D F M F S S
661 GGATGCTGAGATGACTCAACAGATGGATTCCATGACATCTGTGGAACCAACAAGAGCT
-----+-----+-----+-----+-----+-----+-----+
D A G D D S T D G F H D I C G P N K E L

FIG.2B

721 GGATGAGAGACCTGTCAGTGTCTGTCAGAGCGGGCTTCGGCCTGCCAGCTGTGACC
-----+-----+-----+-----+-----+
D E E T C Q C V C R A G L R P A S C G P
781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTA AAAACA AACTCTCCCCAG
-----+-----+-----+-----+-----+
H K E L D R N S C Q C V C K N K L F P S
841 CCAATGTGGGGCCACCAGAAATTGATGAAAACACATGCCAGTGTGTATGTA AAAGAAC
-----+-----+-----+-----+-----+
Q C G A N R E F D E N T C Q C V C K R T
901 CTGCCCCAGAAATCAACCCCTTAATCCTGGA AAATGTGCCCTGTGAATGTACAGAAAGTCC
-----+-----+-----+-----+-----+
C P R N Q P L N P G K C A C E C T E S P
961 ACAGAAATGCTTGTTA AAAGGAAGAGTTCCACCACCAACAACATGCAGCTGTTACAGACC
-----+-----+-----+-----+-----+
Q K C L L K G K K F H H Q T C S C Y R R
1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAGTGTG
-----+-----+-----+-----+-----+
P C T N R Q K A C E P G F S Y S E E V C

FIG. 2C

FIG. 2C is a sequence alignment of the amino acid sequences of the polypeptides encoded by the DNA sequences of the DNA fragments of FIG. 1. The sequences are aligned to show regions of homology. The sequences are: 721 GGATGAGAGACCTGTCAGTGTCTGTCAGAGCGGGCTTCGGCCTGCCAGCTGTGACC, 781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTA AAAACA AACTCTCCCCAG, 841 CCAATGTGGGGCCACCAGAAATTGATGAAAACACATGCCAGTGTGTATGTA AAAGAAC, 901 CTGCCCCAGAAATCAACCCCTTAATCCTGGA AAATGTGCCCTGTGAATGTACAGAAAGTCC, 961 ACAGAAATGCTTGTTA AAAGGAAGAGTTCCACCACCAACAACATGCAGCTGTTACAGACC, 1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAGTGTG. The sequences are aligned to show regions of homology. The sequences are: 721 GGATGAGAGACCTGTCAGTGTCTGTCAGAGCGGGCTTCGGCCTGCCAGCTGTGACC, 781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTA AAAACA AACTCTCCCCAG, 841 CCAATGTGGGGCCACCAGAAATTGATGAAAACACATGCCAGTGTGTATGTA AAAGAAC, 901 CTGCCCCAGAAATCAACCCCTTAATCCTGGA AAATGTGCCCTGTGAATGTACAGAAAGTCC, 961 ACAGAAATGCTTGTTA AAAGGAAGAGTTCCACCACCAACAACATGCAGCTGTTACAGACC, 1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAGTGTG.

1081 TCCTTGTGTCCTTCATATTGCCAAGACCACAATGAGCTAAGATTGTAAGTTTCCCA
-----+-----+-----+-----+-----+-----+
R C V P S Y W Q R P Q M S
+-----+-----+-----+-----+-----+-----+
1141 GTTCATCGATTTTCTATTATGGAAACTGTGTGCCACAGTAGAACTGTCTGTGAACAGA
-----+-----+-----+-----+-----+-----+
1201 GAGACCCCTTGTGGCTCCATGCTAACAAGACAAAAGTCTGTCTTCCCTGAACCATGTGGA
-----+-----+-----+-----+-----+-----+
1261 TAACTTTACAGAAATGAGCTGAGCTCATCTGCAAAAGGCCCTCTGTAAAGACTGTTT
-----+-----+-----+-----+-----+-----+
1321 CTGCCAATGACCAACAGCCAGATTTTCCCTTGATTTCTTAAAGAATGACTATA
-----+-----+-----+-----+-----+-----+
1381 TAATTTATTTCCTAAATAATGTTCTTCGATTCATTTTATAGCAACAATTCGT
-----+-----+-----+-----+-----+-----+
1441 AAAAAGTCACTGTGATCAATATTTTATATCATGCAAAATATGTTTAAATAAATGAAGA
-----+-----+-----+-----+-----+-----+
1501 TTGTATTATATAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+

FIG.2D

1

50

Pdgfa .MRTIACLLL LGGCYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdglb MNRCWA.LFL SLCCYLRIVS AEGDPIPEEL YEMLSDEHIS SPDDLQRLLE
VegfMNFIL SWVHWSLALL LY.....
Vegf2MTV LYPEYWKMKY CQ.....

51

100

Pdgfa IDSVGSEDSL DTSIRAHGVH ATKHVPEKRP LPIRRKRSI.EEAVP
Pdglb GDP.GEEDGA ELDLNMTRSH SGCELES... .LARGRRSLG SLTIAEPAMI
Vegf APMAE..... .GGGQ NHHEVVKFMD .VYQR.....
Vegf2 REQANLNSKT EETIKFAAAH YNTEILKSID NEWRK.....

101

150

Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIMPBC VEVKRCCTGCC NTSVVKCQPS
Pdglb AECRTREVF EISRLIDRT NANFLVMPBC VEVQRCSCCC NNRNVQCRPT
Vegf SYCHPIETLV DIFQYRDEI ..EYIFKPSV VPLMRCGGCC NDEGLECVPT
Vegf2 TCCMPREVCV DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCVNT

151

200

Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.....AT.....
Pdglb QVQLRPQVR KIEIVRKKPI FKKAIVTILED HIAKCK.....ETVAAARPVT
Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLO HNKCECRPKK DRARQEKKSIV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII

FIG. 3A

FIG. 3A

201

250

PdgfaTSINPD YREEDTDVR.
Pdgtb RSPGGSQEQR AKTPQTRVTI RTVRVRBPBK GKHKFKHTH DKTALKEITLG
Vegt RGR..... GKQQRKRK KSRYSWSVY VGARCCIMPW SLPGPH...
Vegt2 RRSIPATLPQ CQANKTCPT NYMNNHICR CLAQEDFMFS SDAGDDSTDG

251

300

Pdgfa
Pdgtb A.....
Vegt ...CGP... ..CSE RKHLFVQDP QTCKSCKNT
Vegt2 FHDICGPKE IDEETCQCVC RAGLRPASC GPHREL..DR NSCQCVCXNK

301

350

Pdgfa
Pdgtb
Vegt ..DSRCKARQ LEINERTCRC DKPRR.....
Vegt2 LFPSQCGANR .EPDENTCQC VCKRTCPRNO PLNPGKACCE CTESPOKCLL

351

398

Pdgfa
Pdgtb
Vegt
Vegt2 KGKKEHHQTC SCYRRPCTNR QKACEPGFSY SEFVCRCVPS YWQRPQMS

FIG. 3B

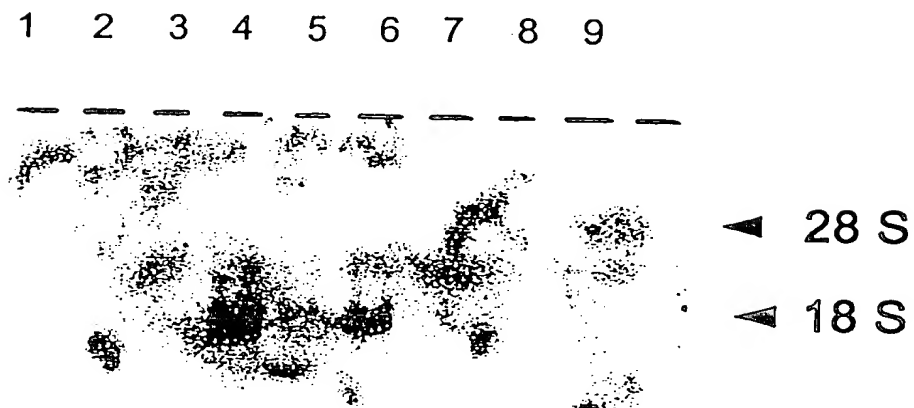
FIG. 3B is a schematic diagram of a system for processing data. The system includes a data source, a processor, and a display. The data source provides input to the processor, which then outputs data to the display. The processor is configured to perform various operations on the input data, such as sorting, filtering, and aggregation. The display shows the results of these operations in a user-friendly format.

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN
EACH PAIR OF GENES IS SHOWN IN THE
FOLLOWING TABLE

	PDGF α	PDGF β	VEGF	VEGF2
PDGF α				
PDGF β	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

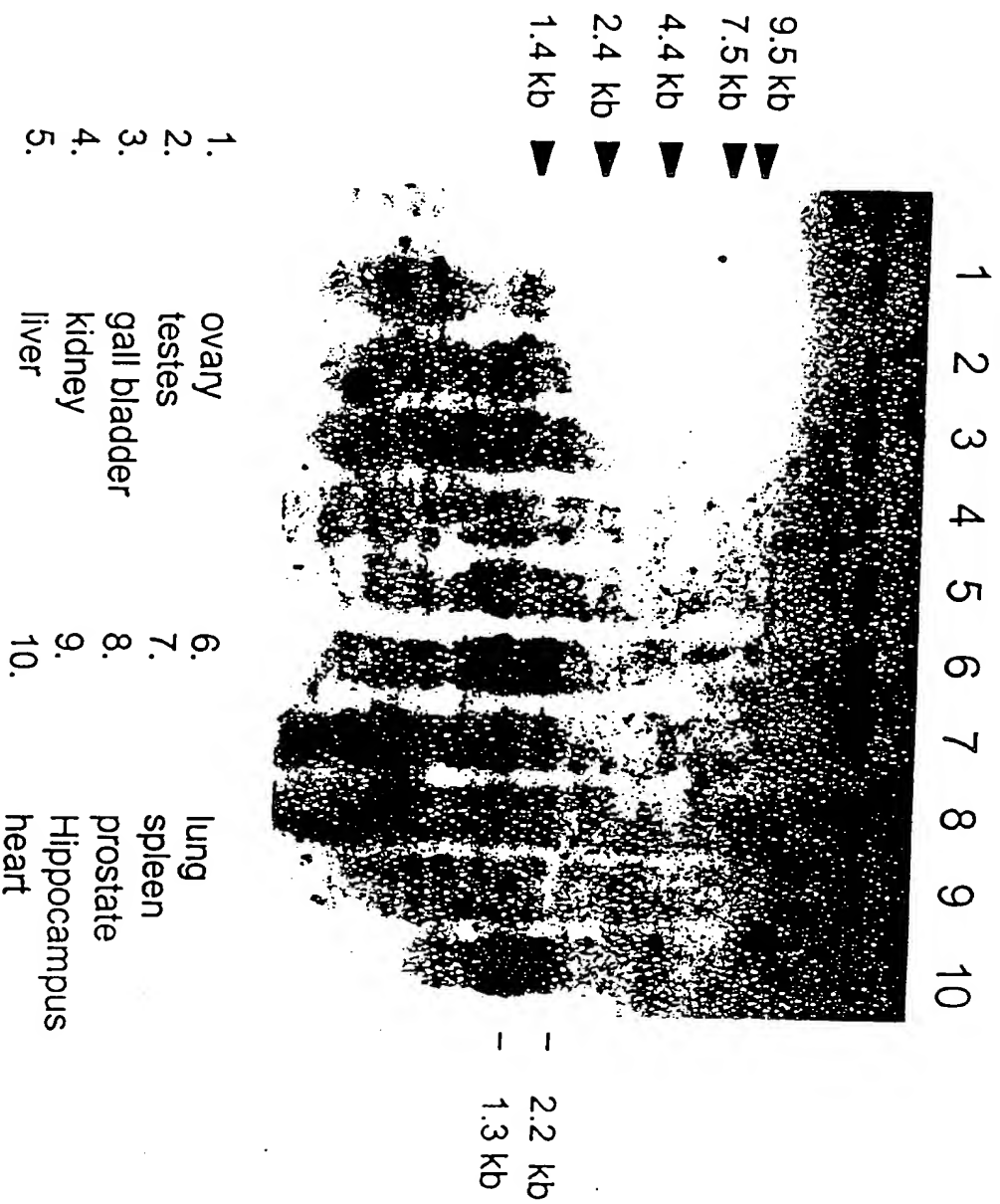
FIG. 4

Expression of VEGF2 mRNA in
Human Breast Tumor Cells



1. normal breast tissue
2. breast tumor tissue
- 3-9. breast tumor cell lines.

FIG. 5

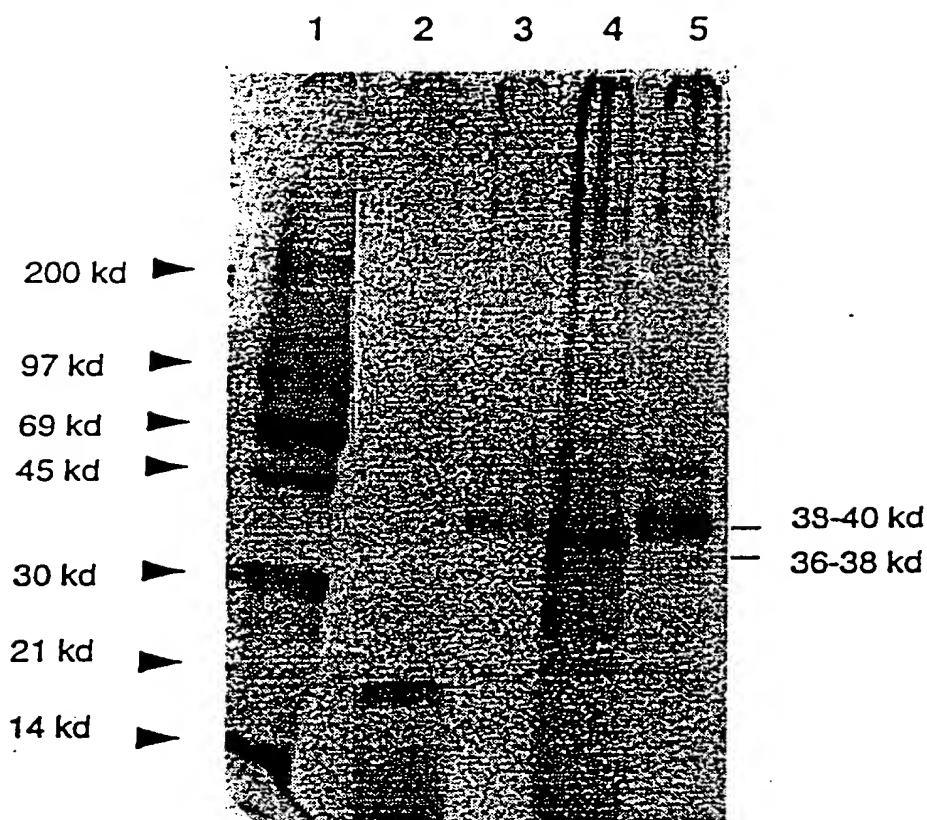


Expression of VEGF2 mRNA in human adult tissues.

FIG. 6

FIG. 6 shows the expression of VEGF2 mRNA in human adult tissues. The tissues are: 1. ovary, 2. testes, 3. gall bladder, 4. kidney, 5. liver, 6. lung, 7. spleen, 8. prostate, 9. Hippocampus, and 10. heart. The molecular weight markers are indicated on the left and right sides of the blot.

FIG. 7



- Lane 1: 14-C and rainbow M.W. marker
- Lane 2: FGF control
- Lane 3: VEGF2 (M13-reverse & forward primers)
- Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
- Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG. 9

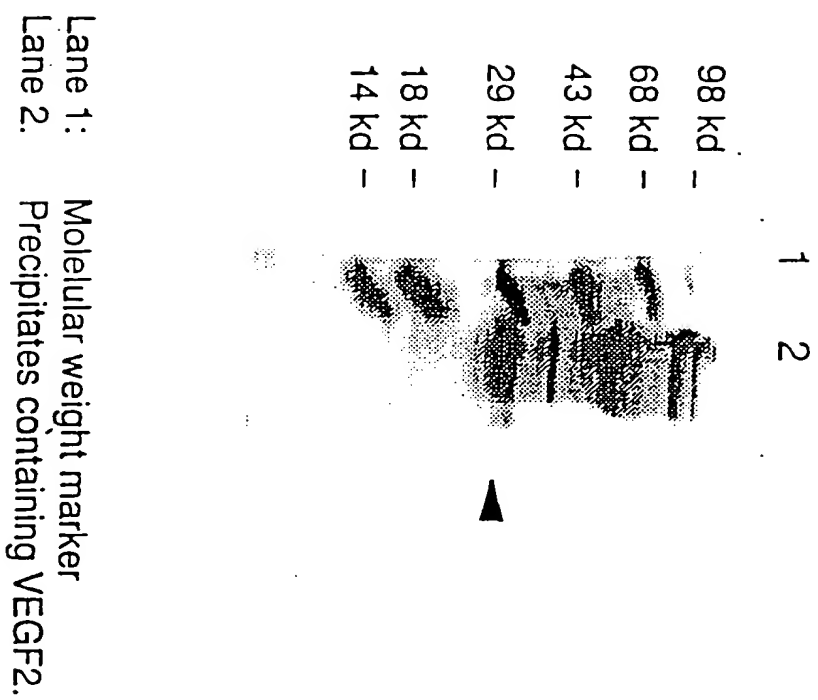


FIG. 10

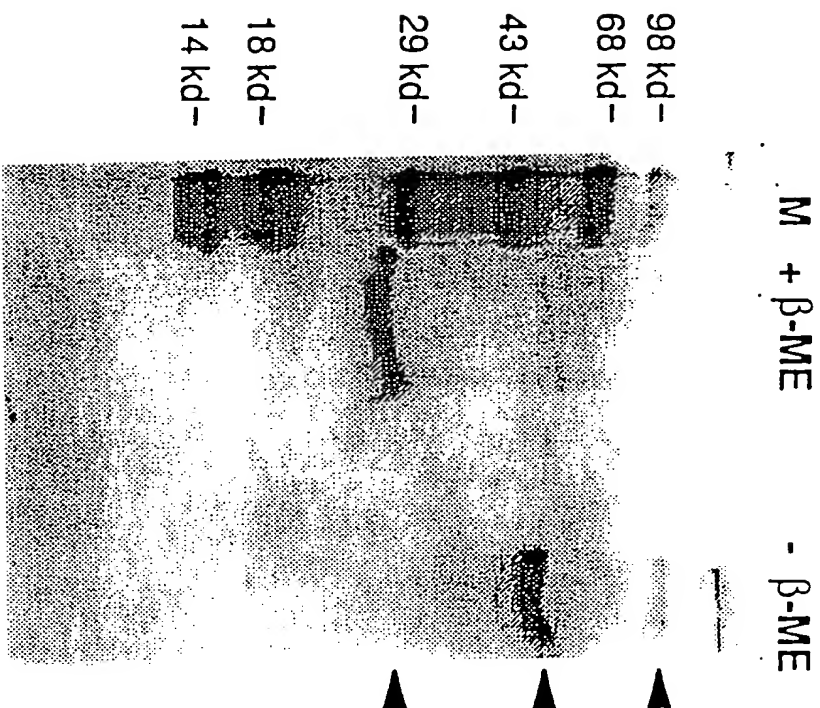


FIG. 11

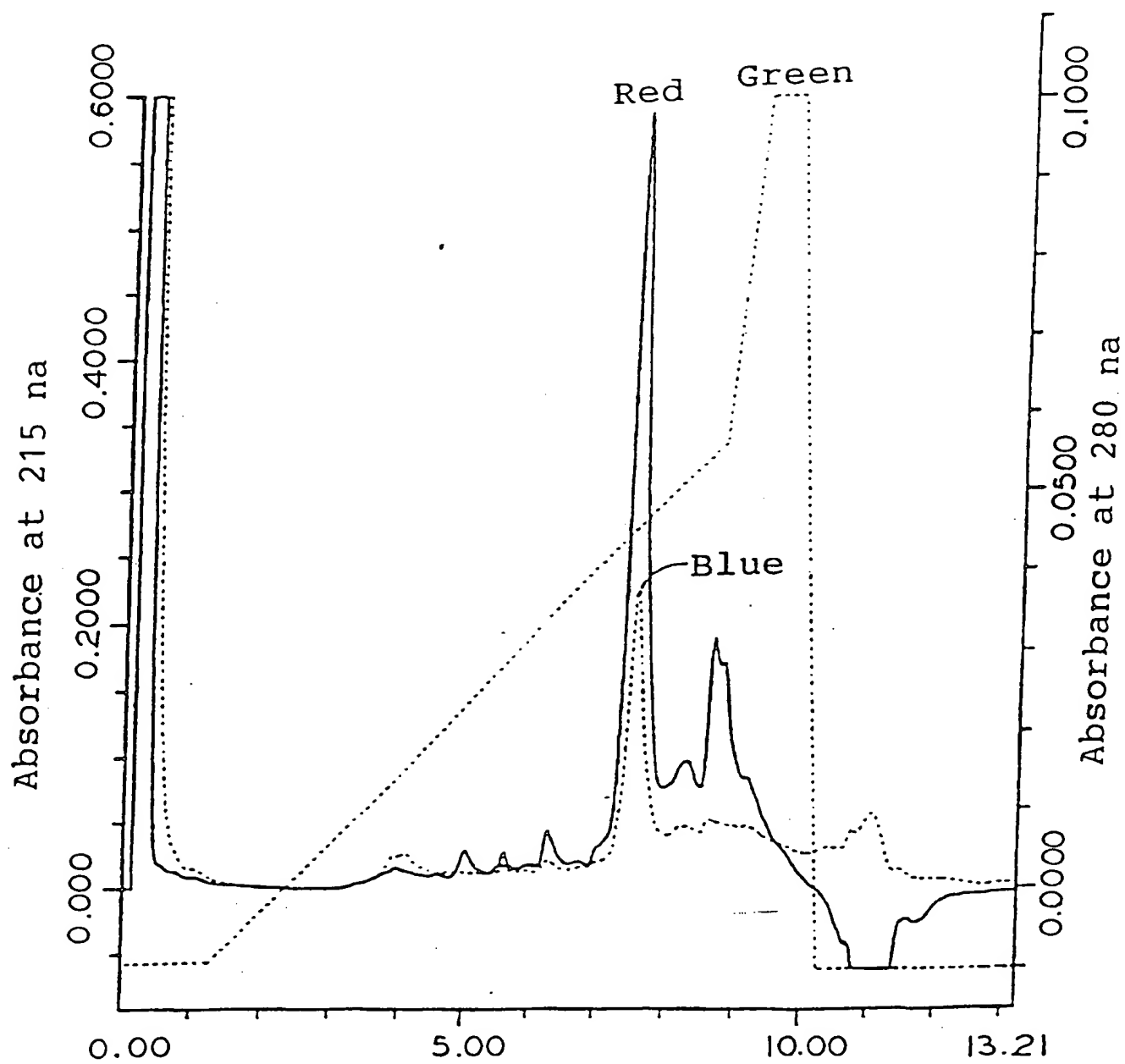


FIG. 12

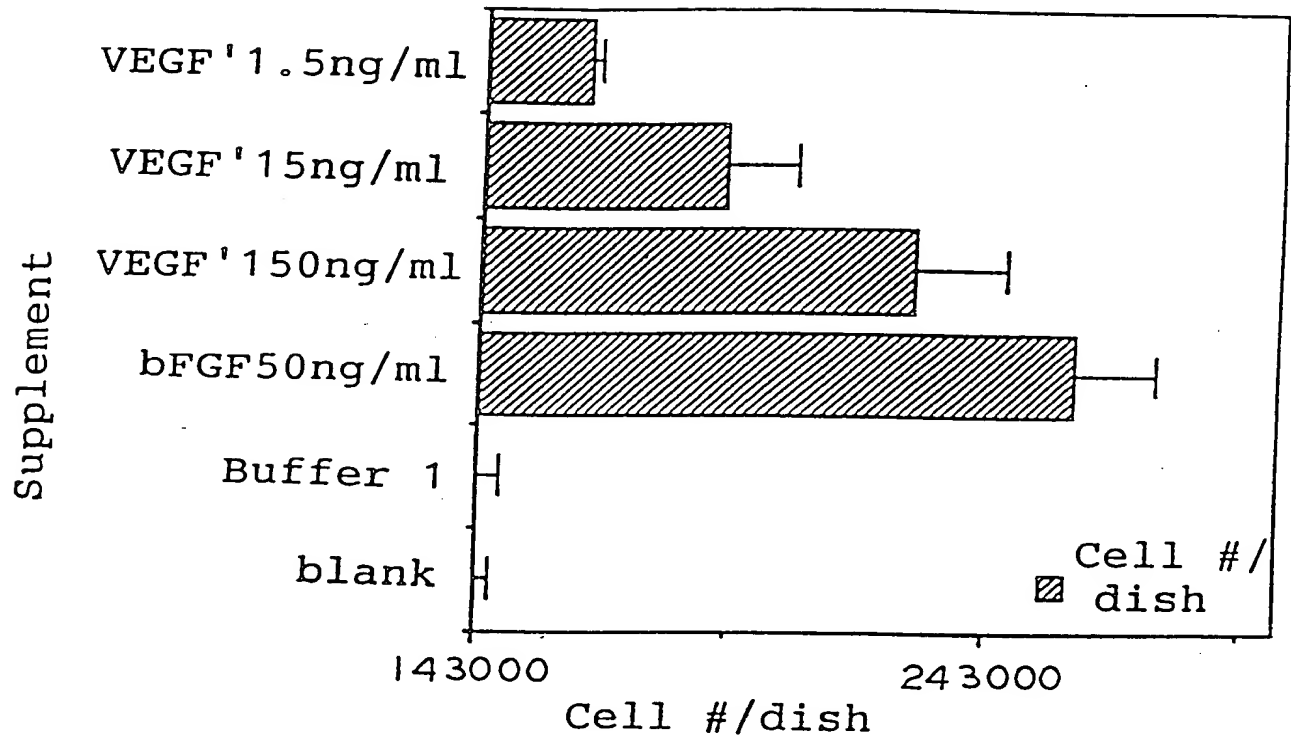


FIG. 13

